BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

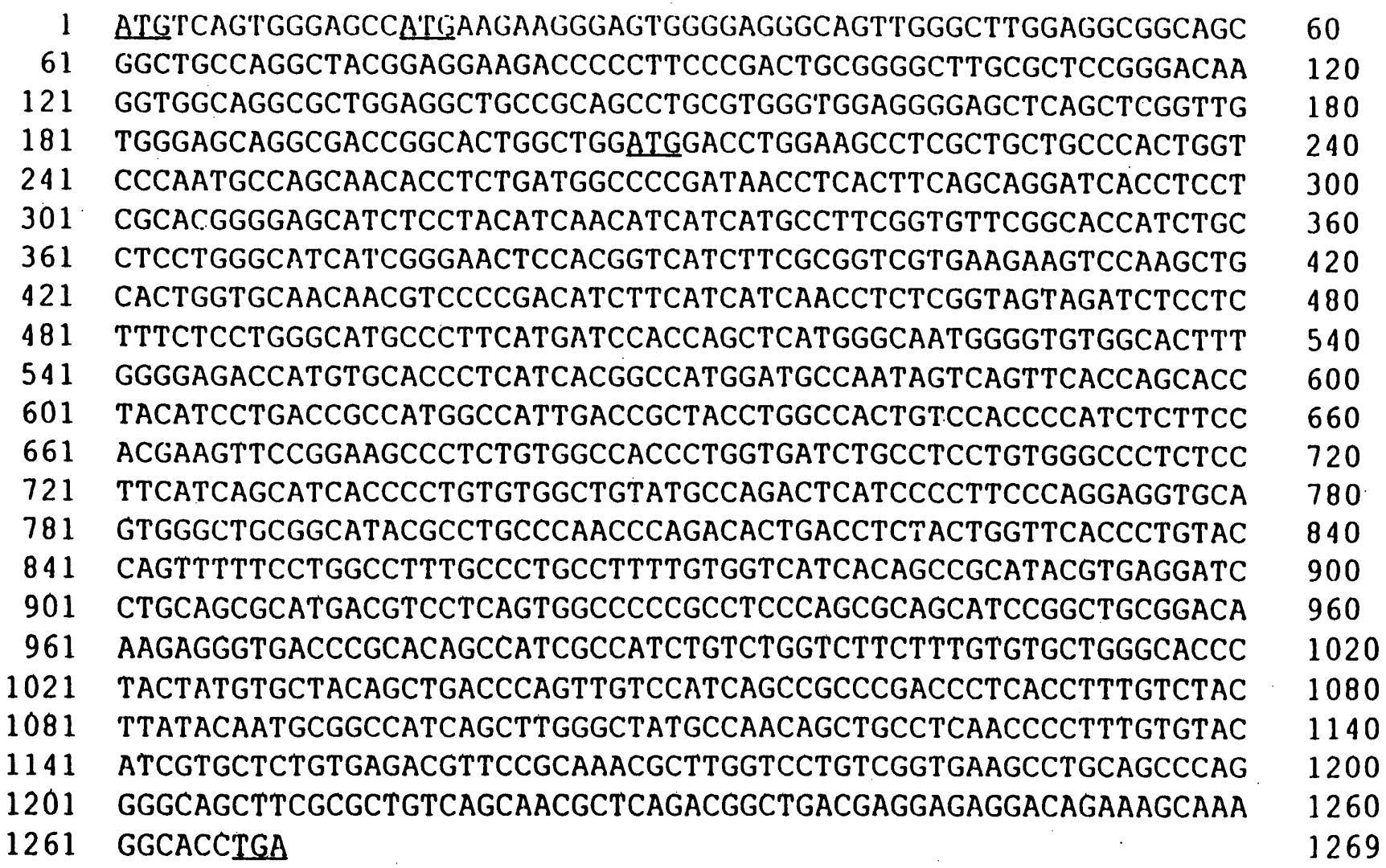
Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images, please do not report the images to the Image Problem Mailbox.

FIGURE 1



Applicants: John A. Salon, et al.
U.S. Serial No.: Not Yet Known
Filed: Herewith
Title: DNA Encoding A Human Melanin Concentrating Hormone Receptor (MCH1) And Uses Thereof
Exhibit B

FIGURE 2

```
  1  M S V G A M K K G V G R A V G L G G G S  20
 21  G C Q A T E E D P L P D C G A C A P G Q  40
 41  G G R R W R L P Q P A W V E G S S A R L  60
 61  W E Q A T G T G W M D L E A S L L P T G  80
 81  P N A S N T S D G P D N L T S A G S P P  100
101  R T G S I S Y I N I I M P S V F G T I C  120
121  L L G I I G N S T V I F A V V K K S K L  140
141  H W C N N V P D I F I I N L S V V D L L  160
161  F L L G M P F M I H Q L M G N G V W H F  180
181  G E T M C T L I T A M D A N S Q F T S T  200
201  Y I L T A M A I D R Y L A T V H P I S S  220
221  T K F R K P S V A T L V I C L L W A L S  240
241  F I S I T P V W L Y A R L I P F P G G A  260
261  V G C G I R L P N P D T D L Y W F T L Y  280
281  Q F F L A F A L P F V V I T A A Y V R I  300
301  L Q R M T S S V A P A S Q R S I R L R T  320
321  K R V T R T A I A I C L V F F V C W A P  340
341  Y Y V L Q L T Q L S I S R P T L T F V Y  360
361  L Y N A A I S L G Y A N S C L N P F V Y  380
381  I V L C E T F R K R L V L S V K P A A Q  400
401  G Q L R A V S N A Q T A D E E R T E S K  420
421  G T                                    422
```

FIGURE 3

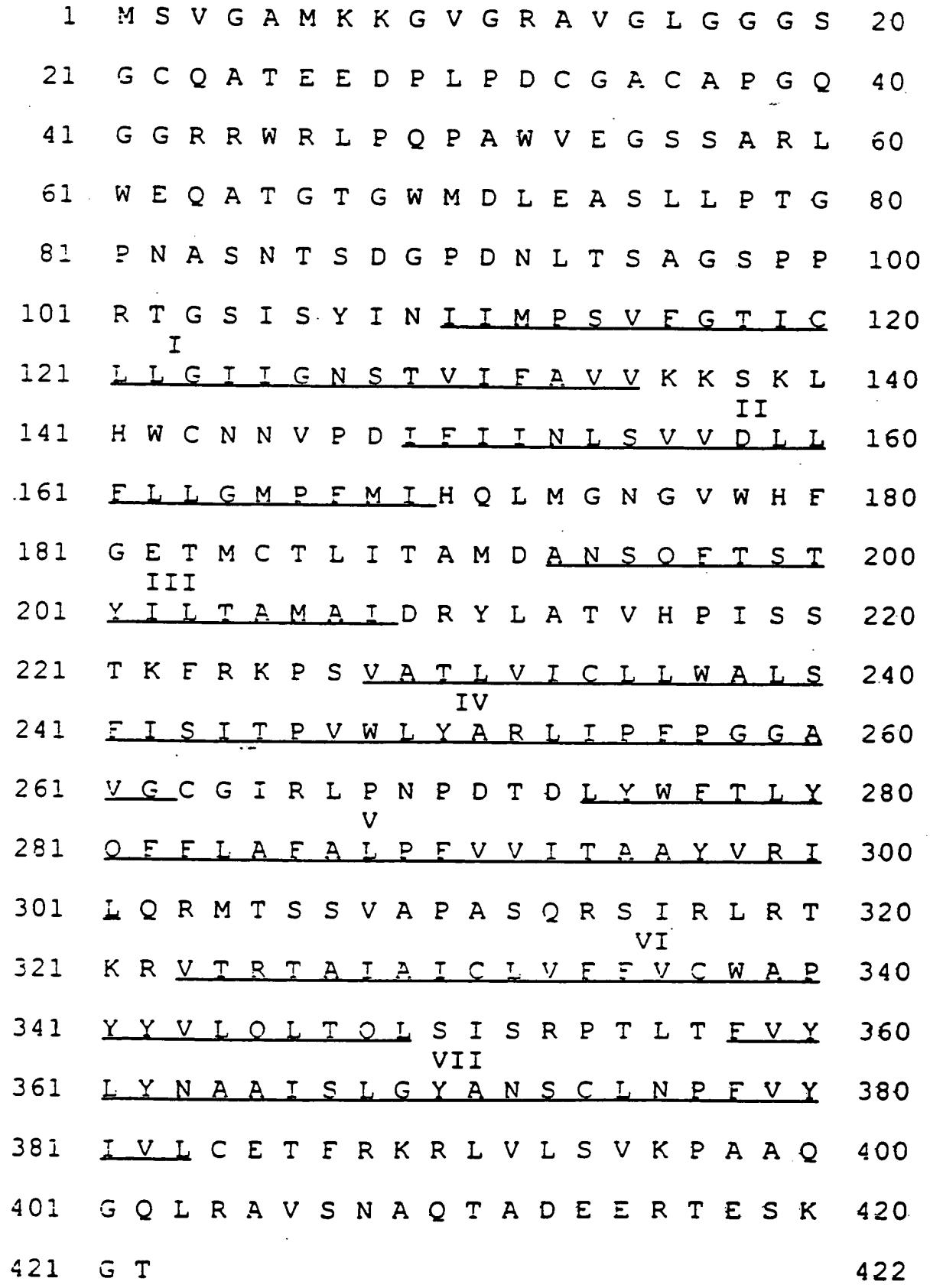

1 M S V G A M K K G V G R A V G L G G G S 20
21 G C Q A T E E D P L P D C G A C A P G Q 40
41 G G R R W R L P Q P A W V E G S S A R L 60
61 W E Q A T G T G W M D L E A S L L P T G 80
81 P N A S N T S D G P D N L T S A G S P P 100
101 R T G S I S Y I N I I M P S V F G T I C 120
I
121 L L G I I G N S T V I F A V V K K S K L 140
II
141 H W C N N V P D I F I I N L S V V D L L 160
161 F L L G M P F M I H Q L M G N G V W H F 180
181 G E T M C T L I T A M D A N S Q F T S T 200
III
201 Y I L T A M A I D R Y L A T V H P I S S 220
221 T K F R K P S V A T L V I C L L W A L S 240
IV
241 F I S I T P V W L Y A R L I P F P G G A 260
261 V G C G I R L P N P D T D L Y W F T L Y 280
V
281 Q F F L A F A L P F V V I T A A Y V R I 300
301 L Q R M T S S V A P A S Q R S I R L R T 320
VI
321 K R V T R T A I A I C L V F F V C W A P 340
341 Y Y V L Q L T Q L S I S R P T L T F V Y 360
VII
361 L Y N A A I S L G Y A N S C L N P F V Y 380
381 I V L C E T F R K R L V L S V K P A A Q 400
401 G Q L R A V S N A Q T A D E E R T E S K 420
421 G T 422

FIGURE 4

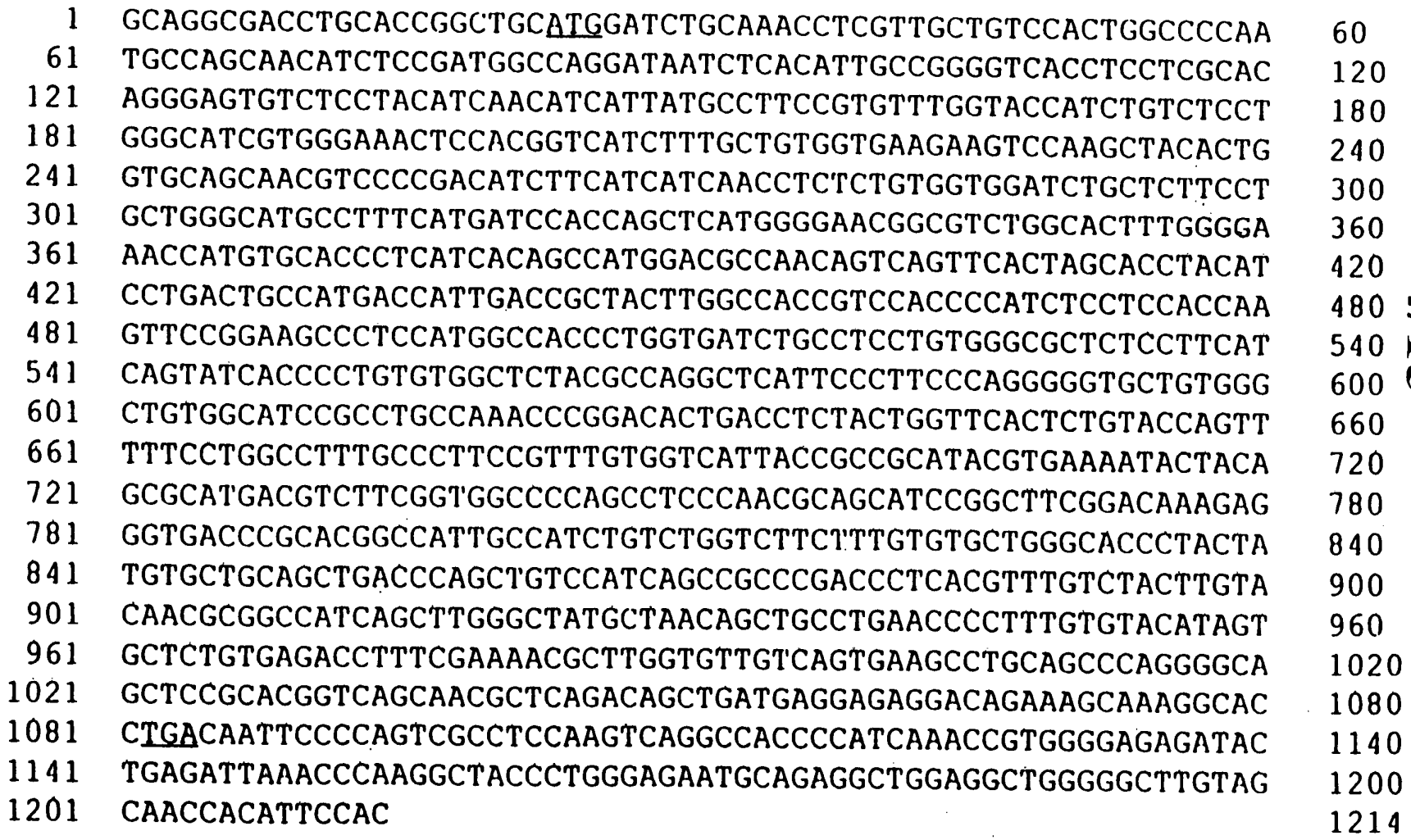

1 GCAGGCGACCTGCACCGGCTGCATGGATCTGCAAACCTCGTTGCTGTCCACTGGCCCCAA 60
61 TGCCAGCAACATCTCCGATGGCCAGGATAATCTCACATTGCCGGGGTCACCTCCTCGCAC 120
121 AGGGAGTGTCTCCTACATCAACATCATTATGCCTTCCGTGTTTGGTACCATCTGTCTCCT 180
181 GGGCATCGTGGGAAACTCCACGGTCATCTTTGCTGTGGTGAAGAAGTCCAAGCTACACTG 240
241 GTGCAGCAACGTCCCCGACATCTTCATCATCAACCTCTCTGTGGTGGATCTGCTCTTCCT 300
301 GCTGGGCATGCCTTTCATGATCCACCAGCTCATGGGGAACGGCGTCTGGCACTTTGGGGA 360
361 AACCATGTGCACCCTCATCACAGCCATGGACGCCAACAGTCAGTTCACTAGCACCTACAT 420
421 CCTGACTGCCATGACCATTGACCGCTACTTGGCCACCGTCCACCCCATCTCCTCCACCAA 480
481 GTTCCGGAAGCCCTCCATGGCCACCCTGGTGATCTGCCTCCTGTGGGCGCTCTCCTTCAT 540
541 CAGTATCACCCCTGTGTGGCTCTACGCCAGGCTCATTCCCTTCCCAGGGGGTGCTGTGGG 600
601 CTGTGGCATCCGCCTGCCAAACCCGGACACTGACCTCTACTGGTTCACTCTGTACCAGTT 660
661 TTTCCTGGCCTTTGCCCTTCCGTTTGTGGTCATTACCGCCGCATACGTGAAAATACTACA 720
721 GCGCATGACGTCTTCGGTGGCCCCAGCCTCCCAACGCAGCATCCGGCTTCGGACAAAGAG 780
781 GGTGACCCGCACGGCCATTGCCATCTGTCTGGTCTTCTTTGTGTGCTGGGCACCCTACTA 840
841 TGTGCTGCAGCTGACCCAGCTGTCCATCAGCCGCCCGACCCTCACGTTTGTCTACTTGTA 900
901 CAACGCGGCCATCAGCTTGGGCTATGCTAACAGCTGCCTGAACCCCTTTGTGTACATAGT 960
961 GCTCTGTGAGACCTTTCGAAAACGCTTGGTGTTGTCAGTGAAGCCTGCAGCCCAGGGGCA 1020
1021 GCTCCGCACGGTCAGCAACGCTCAGACAGCTGATGAGGAGAGGACAGAAAGCAAAGGCAC 1080
1081 CTGACAATTCCCCAGTCGCCTCCAAGTCAGGCCACCCCATCAAACCGTGGGGAGAGATAC 1140
1141 TGAGATTAAACCCAAGGCTACCCTGGGAGAATGCAGAGGCTGGAGGCTGGGGGCTTGTAG 1200
1201 CAACCACATTCCAC 1214

FIGURE 5

```
  1  M D L Q T S L L S T G P N A S N I S D G  20
 21  Q D N L T L P G S P P R T G S V S Y I N  40
 41  I I M P S V F G T I C L L G I V G N S T  60
 61  V I F A V V K K S K L H W C S N V P D I  80
 81  F I I N L S V V D L L F L L G M P F M I 100
101  H Q L M G N G V W H F G E T M C T L I T 120
121  A M D A N S Q F T S T Y I L T A M T I D 140
141  R Y L A T V H P I S S T K F R K P S M A 160
161  T L V I C L L W A L S F I S I T P V W L 180
181  Y A R L I P F P G G A V G C G I R L P N 200
201  P D T D L Y W F T L Y Q F F L A F A L P 220
221  F V V I T A A Y V K I L Q R M T S S V A 240
241  P A S Q R S I R L R T K R V T R T A I A 260
261  I C L V F F V C W A P Y Y V L Q L T Q L 280
281  S I S R P T L T F V Y L Y N A A I S L G 300
301  Y A N S C L N P F V Y I V L C E T F R K 320
321  R L V L S V K P A A Q G Q L R T V S N A 340
341  Q T A D E E R T E S K G T *             354
```

FIGURE 6

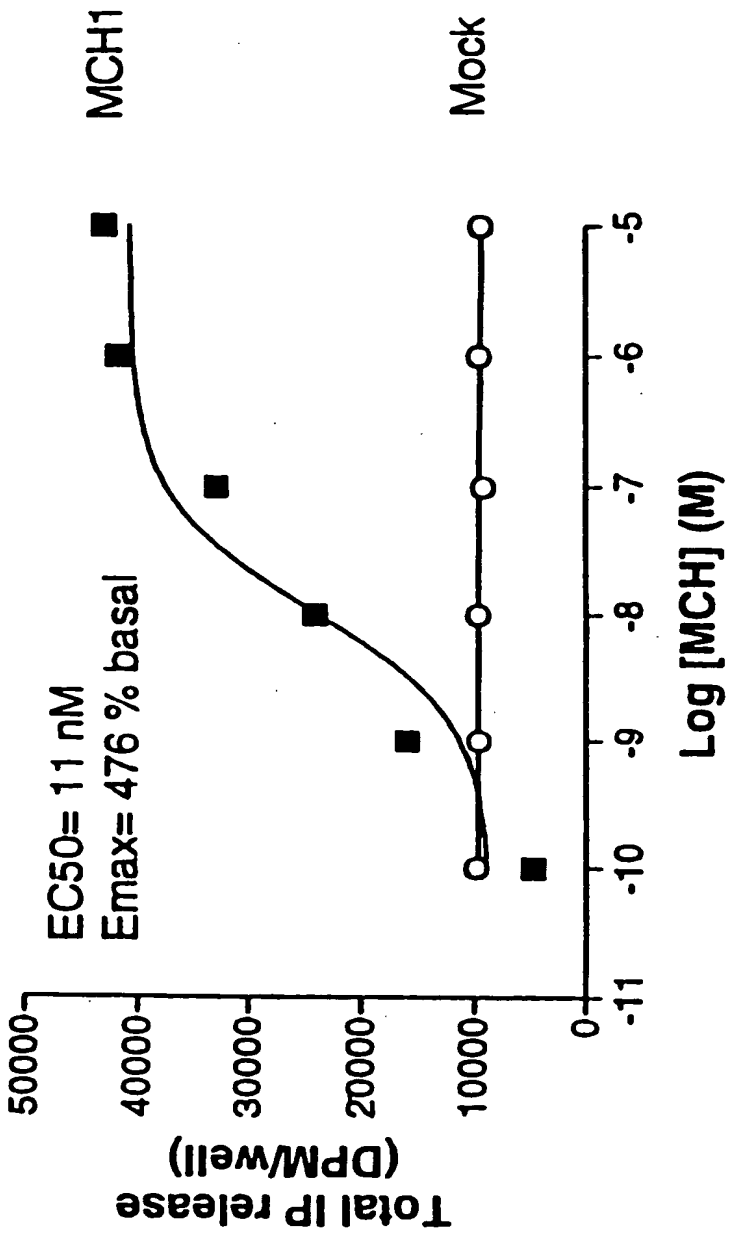

IP release in MCH1- and mock-transfected Cos-7 cells
EC50= 11 nM
Emax= 476 % basal
MCH1
Mock
Total IP release (DPM/well)
50000
40000
30000
20000
10000
0
-11
-10
-9
-8
-7
-6
-5
Log [MCH] (M)

FIGURE 7A

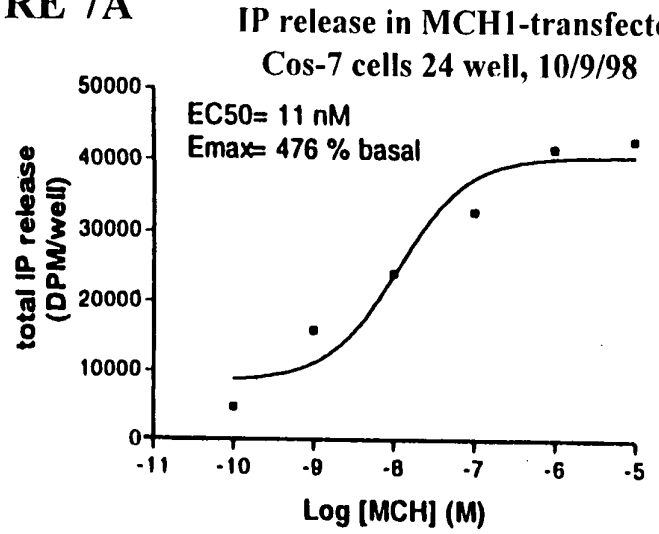


FIGURE 7B

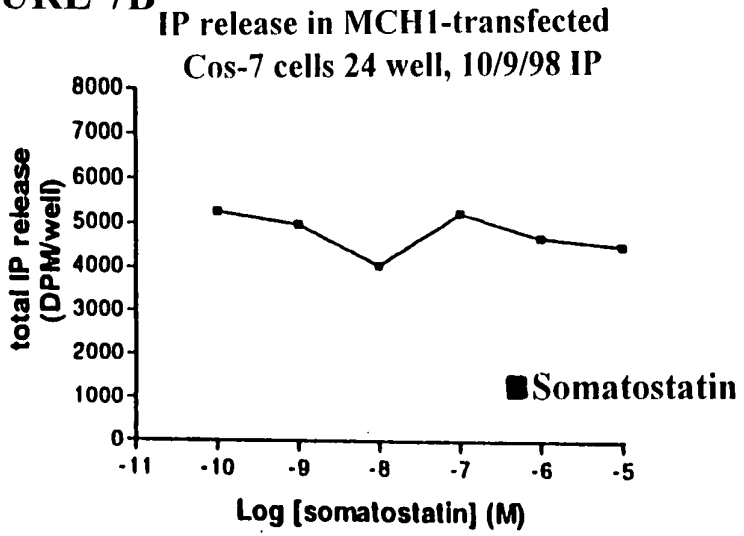


FIGURE 7C

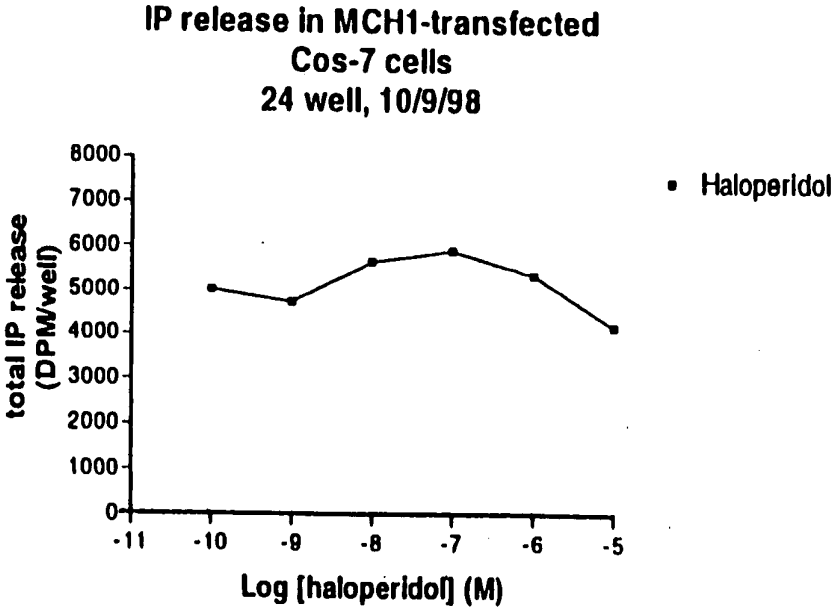


FIGURE 7D

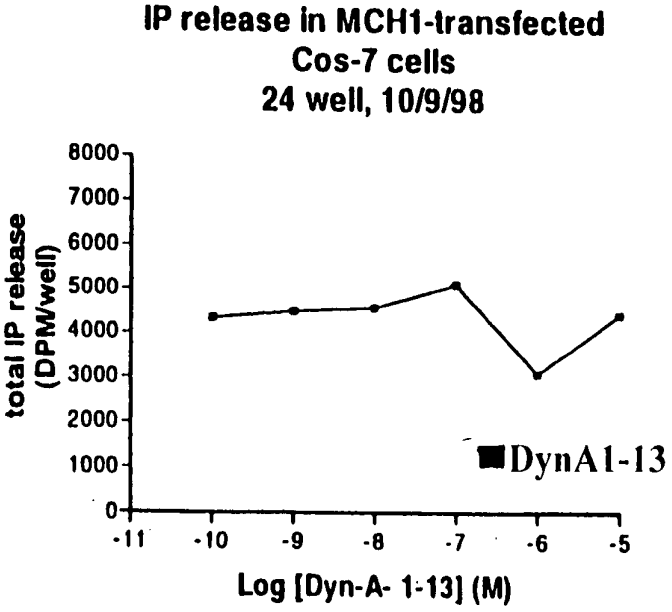


FIGURE 8A

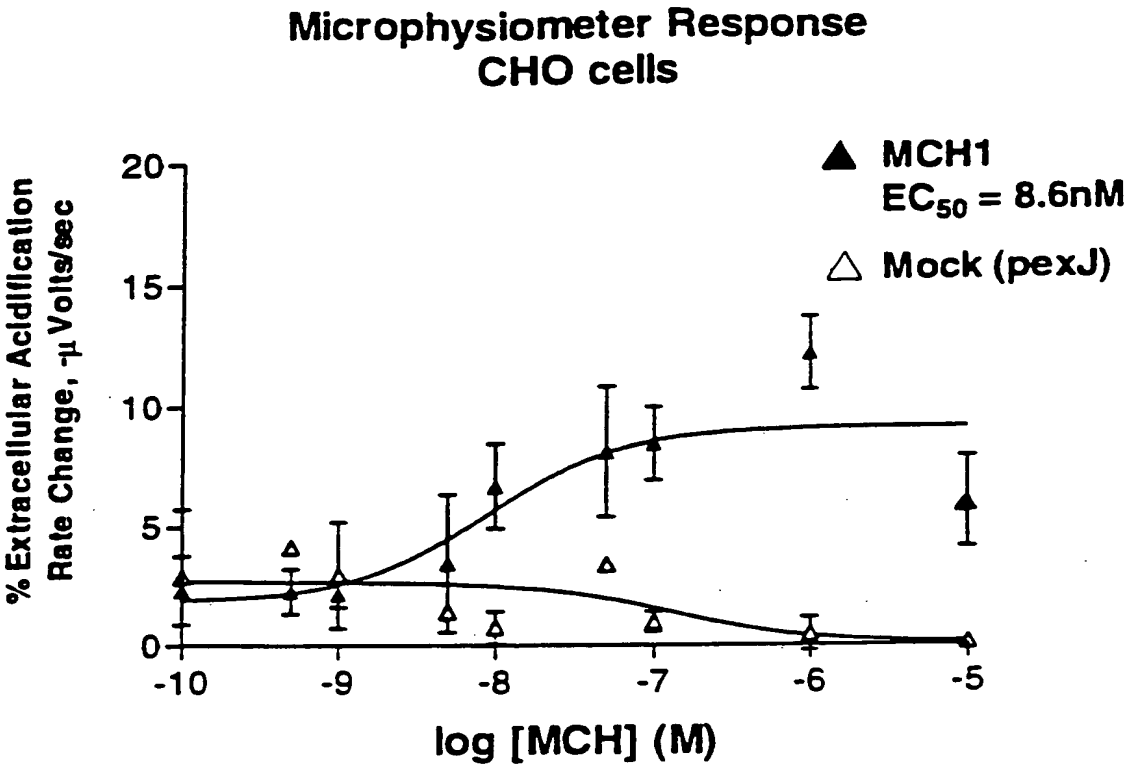


FIGURE 8B

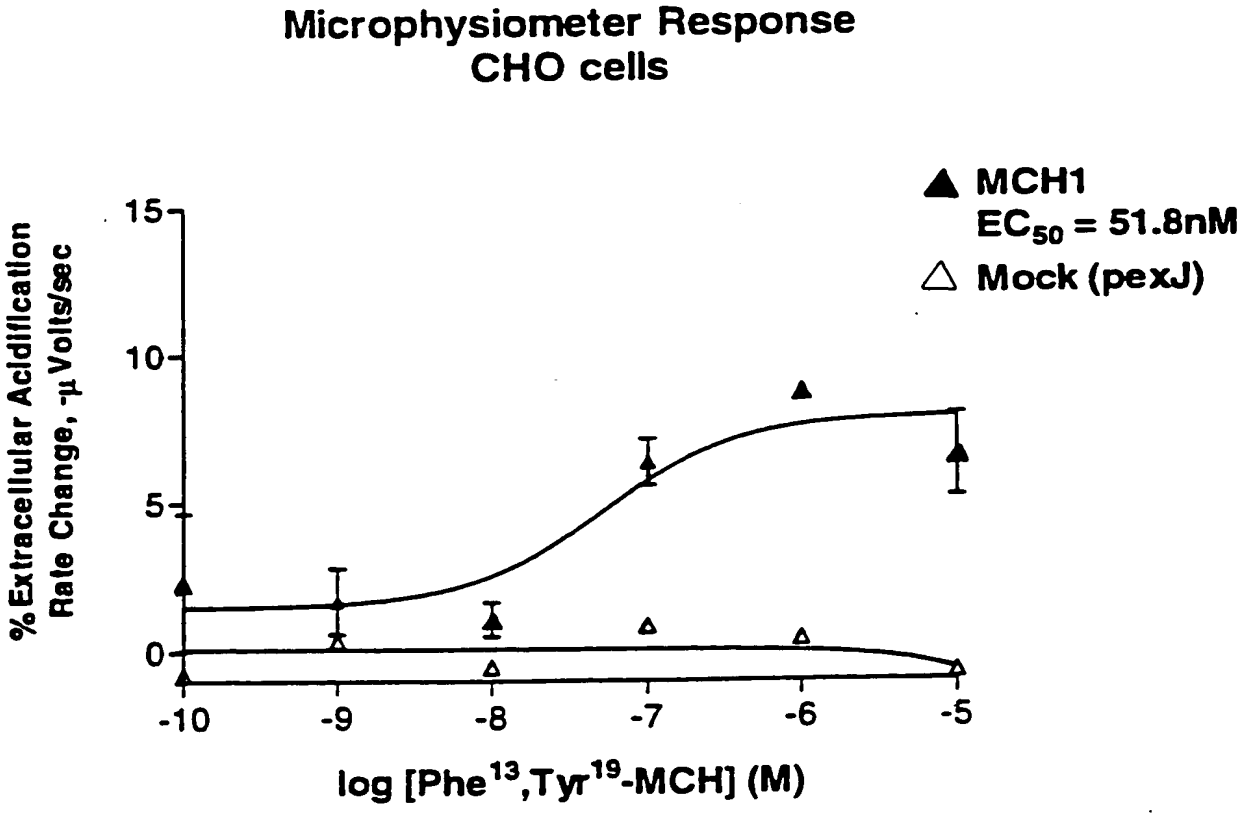


FIGURE 9

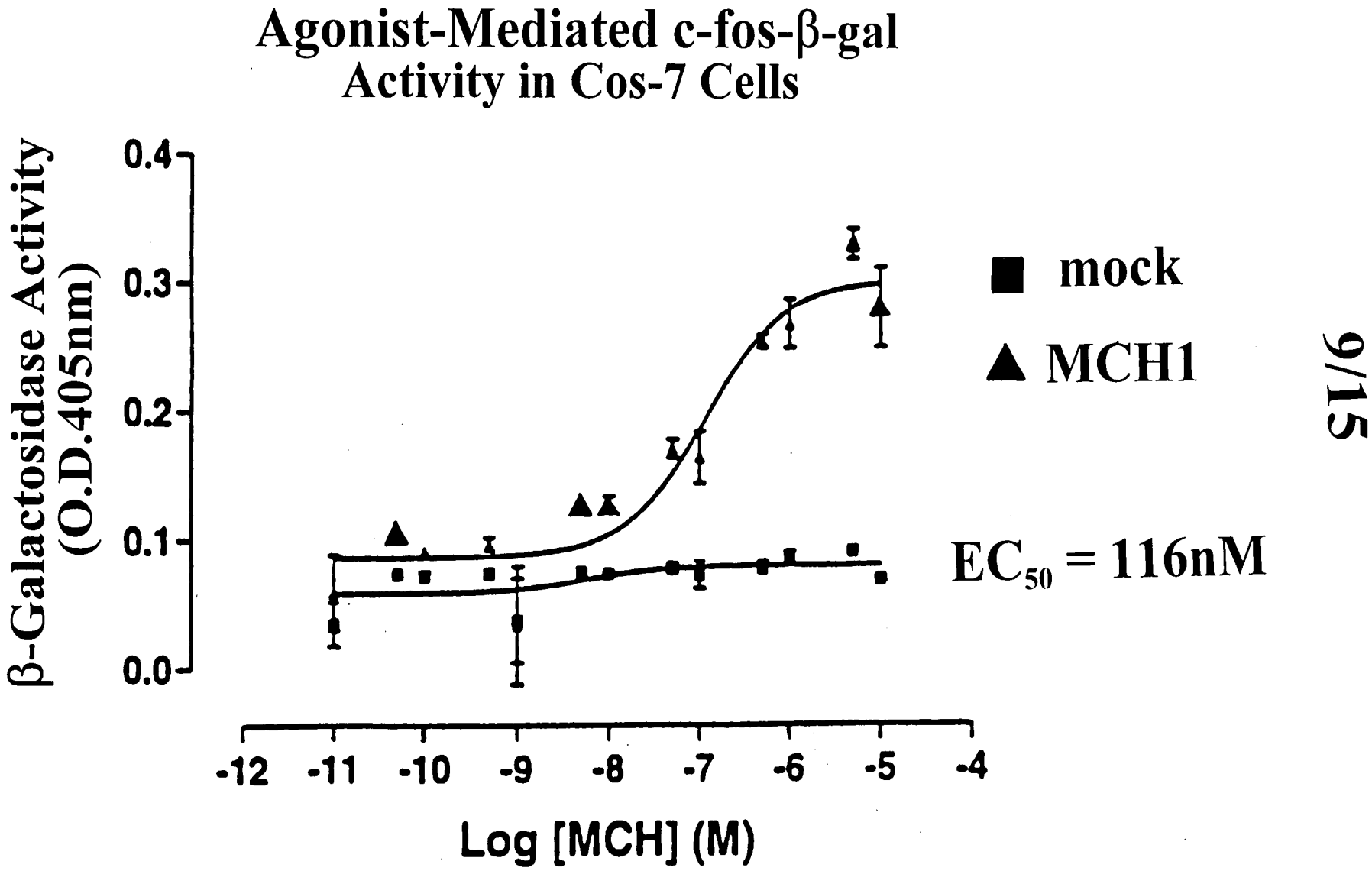

Agonist-Mediated c-fos-β-gal
Activity in Cos-7 Cells
β-Galactosidase Activity
(O.D.405nm)
0.4
0.3
0.2
0.1
0.0
-12
-11
-10
-9
-8
-7
-6
-5
-4
Log [MCH] (M)
mock
MCH1
EC50 = 116nM

FIGURE 10A

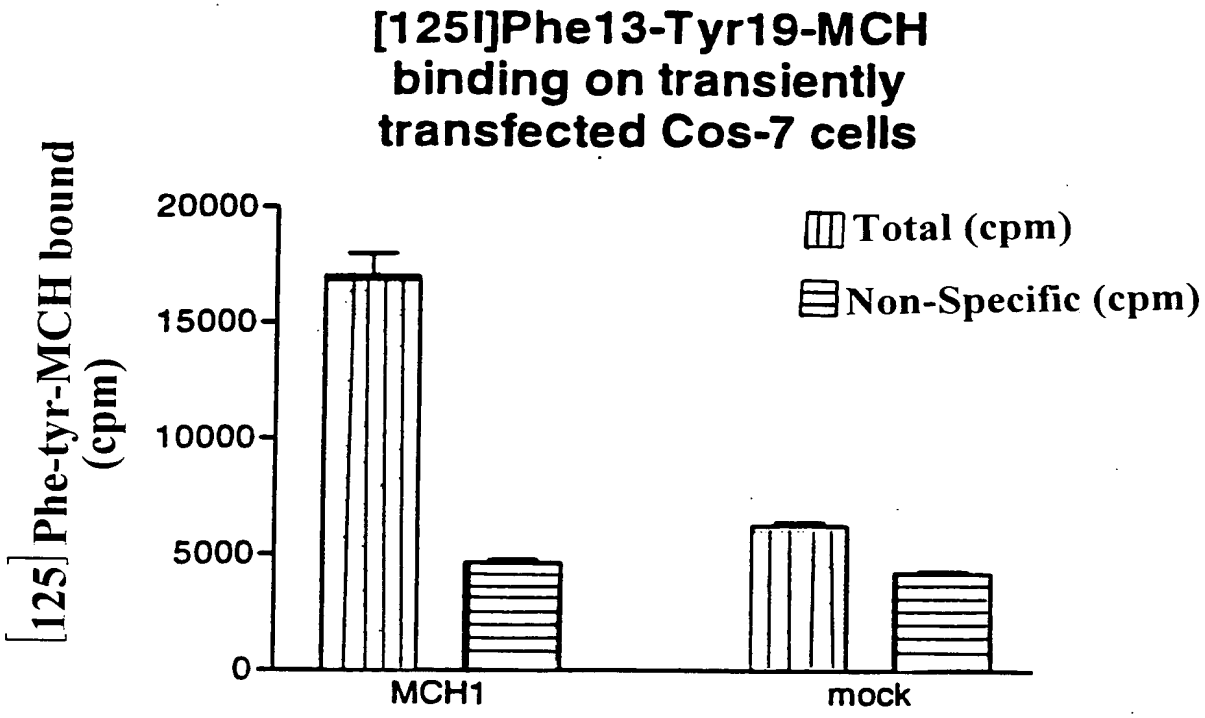


FIGURE 10B

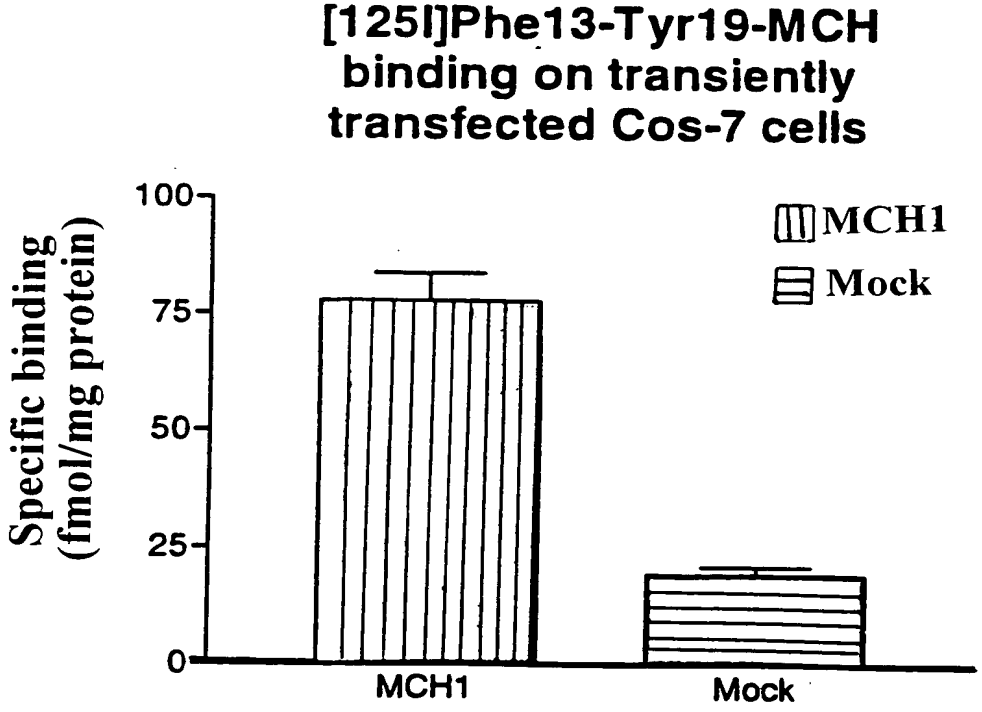


FIGURE 11

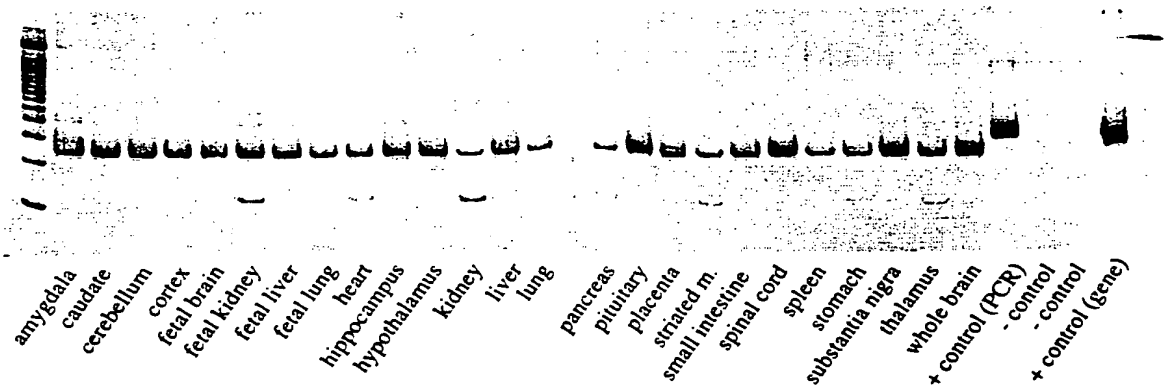

amygdala
caudate
cerebellum
cortex
fetal brain
fetal kidney
fetal liver
fetal lung
heart
hippocampus
hypothalamus
kidney
liver
lung
pancreas
pituitary
placenta
striated m.
small intestine
spinal cord
spleen
stomach
substantia nigra
thalamus
whole brain
+ control (PCR)
- control
- control
+ control (gene)

FIGURE 12

```
                1                                                  40
TL231           MSVGAMKKGV  GRAVGLGGGS  GCQATEEDPL  PDCGACAPGQ
R106            MSVGAMKKGV  GRAVGLGGGS  GCQATEEDPL  PDCGACAPGQ
R114            MSVGAaKKGV  GRAVGLGGGS  GCQATEEDPL  PDCGACAPGQ
BO120           ~~~~~~~~~~  ~~~~~~~~~~  ~~~~~~~~~~  ~~~~~~~~~~

                41                                                 80
TL231           GGRRWRLPQP  AWVEGSSARL  WEQATGTGWM  DLEASLLPTG
R106            GGRRWRLPQP  AWVEGSSARL  WEQATGTGWa  DLEASLLPTG
R114            GGRRWRLPQP  AWVEGSSARL  WEQATGTGWa  DLEASLLPTG
BO120           ~~~~~~~~~~  ~~~~~~~~~~  ~~~~~~~~~~M DLEASLLPTG

                81                  100
TL231           PNASNTSDGP  DNLTSAGSPP...
R106            PNASNTSDGP  DNLTSAGSPP...
R114            PNASNTSDGP  DNLTSAGSPP...
BO120           PNASNTSDGP  DNLTSAGSPP...
```

FIGURE 13

```
  1  M S V G A M K K G V G R A V G L G G G S  20
 21  G C Q A T E E D P L P D C G A C A P G Q  40
 41  G G R R W R L P Q P A W V E G S S A R L  60
 61  W E Q A T G T G W A D L E A S L L P T G  80
 81  P N A S N T S D G P D N L T S A G S P P 100
101  R T G S I S Y I N I I M P S V F G T I C 120
121  L L G I I G N S T V I F A V V K K S K L 140
141  H W C N N V P D I F I I N L S V V D L L 160
161  F L L G M P F M I H Q L M G N G V W H F 180
181  G E T M C T L I T A M D A N S Q F T S T 200
201  Y I L T A M A I D R Y L A T V H P I S S 220
221  T K F R K P S V A T L V I C L L W A L S 240
241  F I S I T P V W L Y A R L I P F P G G A 260
261  V G C G I R L P N P D T D L Y W F T L Y 280
281  Q F F L A F A L P F V V I T A A Y V R I 300
301  L Q R M T S S V A P A S Q R S I R L R T 320
321  K R V T R T A I A I C L V F F V C W A P 340
341  Y Y V L Q L T Q L S I S R P T L T F V Y 360
361  L Y N A A I S L G Y A N S C L N P F V Y 380
381  I V L C E T F R K R L V L S V K P A A Q 400
401  G Q L R A V S N A Q T A D E E R T E S K 420
421  G T                                   422
```

FIGURE 14

```
  1  M S V G A A K K G V G R A V G L G G G S  20
 21  G C Q A T E E D P L P D C G A C A P G Q  40
 41  G G R R W R L P Q P A W V E G S S A R L  60
 61  W E Q A T G T G W A D L E A S L L P T G  80
 81  P N A S N T S D G P D N L T S A G S P P 100
101  R T G S I S Y I N I I M P S V F G T I C 120
121  L L G I I G N S T V I F A V V K K S K L 140
141  H W C N N V P D I F I I N L S V V D L L 160
161  F L L G M P F M I H Q L M G N G V W H F 180
181  G E T M C T L I T A M D A N S Q F T S T 200
201  Y I L T A M A I D R Y L A T V H P I S S 220
221  T K F R K P S V A T L V I C L L W A L S 240
241  F I S I T P V W L Y A R L I P F P G G A 260
261  V G C G I R L P N P D T D L Y W F T L Y 280
281  Q F F L A F A L P F V V I T A A Y V R I 300
301  L Q R M T S S V A P A S Q R S I R L R T 320
321  K R V T R T A I A I C L V F F V C W A P 340
341  Y Y V L Q L T Q L S I S R P T L T F V Y 360
361  L Y N A A I S L G Y A N S C L N P F V Y 380
381  I V L C E T F R K R L V L S V K P A A Q 400
401  G Q L R A V S N A Q T A D E E R T E S K 420
421  G T                                   422
```

FIGURE 15

```
  1  M D L E A S L L P T G P N A S N T S D G  20
 21  P D N L T S A G S P P R T G S I S Y I N  40
 41  I I M P S V F G T I C L L G I I G N S T  60
 61  V I F A V V K K S K L H W C N N V P D I  80
 81  F I I N L S V V D L L F L L G M P F M I 100
101  H Q L M G N G V W H F G E T M C T L I T 120
121  A M D A N S Q F T S T Y I L T A M A I D 140
141  R Y L A T V H P I S S T K F R K P S V A 160
161  T L V I C L L W A L S F I S I T P V W L 180
181  Y A R L I P F P G G A V G C G I R L P N 200
201  P D T D L Y W F T L Y Q F F L A F A L P 220
221  F V V I T A A Y V R I L Q R M T S S V A 240
241  P A S Q R S I R L R T K R V T R T A I A 260
261  I C L V F F V C W A P Y Y V L Q L T Q L 280
281  S I S R P T L T F V Y L Y N A A I S L G 300
301  Y A N S C L N P F V Y I V L C E T F R K 320
321  R L V L S V K P A A Q G Q L R A V S N A 340
341  Q T A D E E R T E S K G T               353
```